BLAST Basic Local Alignment Search Tool

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BLASTN programs search nucleotide subjects using a nucleotide query. more...

Reset page Bookmark

---Enter Query Sequence---

Enter accession number, gi, or FASTA sequence [?] Clear

Query sequence(s) to be used for a BLAST search should be pasted in the text area. It automatically determines the format or the input. To allow this feature there are certain conventions required with regard to the input of identifiers. more...

NM_022162

Query subrange [?]

From

To [   ]

Enter coordinates for a **subrange** of the query sequence. The BLAST search will apply only to the residues in the range. Sequence coordinates are from 1 to the sequence length.The range includes the residue at the **To** coordinate. more...

Or, upload file

[   ] [Browse..] [?]

Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.

Genetic code

[Standard (1)   ▼]

Job Title

[NM_022162:Homo sapiens nucleotide-binding...]

Enter a descriptive title for your BLAST search [?]

This title appears on all BLAST results and saved searches.

☑ Align two or more sequences [?]

To get the CDS annotation in the output, use only the NCBI accession or gi number for either the query or subject. Reformat the results and check 'CDS feature' to display that annotation.

Enter Subject Sequence

Enter accession number, gi, or FASTA sequence [?] Clear

Subject sequence(s) to be used for a BLAST search should be pasted in the text area. It automatically determines the format or the input. To allow this feature there are certain conventions required with regard to the input of identifiers. more...

[AC007728   ▒]
[   ]
[▒]

Subject subrange [?]

From [   ]

To [   ]

Enter coordinates for a **subrange** of the subject sequence. The BLAST search will apply only to the residues in the range. Sequence coordinates are from 1 to the sequence length.The range includes the residue at the **To** coordinate. more...

Or, upload file

[   ] Browse... [?]

Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.

Choose Search Set

Database

⊙ Human genomic + transcript   ○ Mouse genomic + transcript   ○ Others (nr etc.):

[Human genomic plus transcript (Human G+T) ▼] [?]

Select the sequence database to run searches against. No BLAST database contains all the sequences at NCBI. BLAST databases are organized by informational content (nr, RefSeq, etc.) or by sequencing technique (WGS, EST, etc.). more...

Organism

Optional

[Enter organism name or id--completions will be suggested]

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?]

Select from the list or choose "Custom" to enter the name of an organism. The search will be restricted to the sequences in the database which are from the organism selected.

Entrez Query

Optional

[   ]

Enter an Entrez query to limit search [?]

You can use Entrez query syntax to search a subset of the selected BLAST database. This can be helpful to limit searches to molecule types, sequence lengths or to exclude organisms. more...

Program Selection

Optimize for

○ Highly similar sequences (megablast)

○ More dissimilar sequences (discontiguous megablast)

⊙ Somewhat similar sequences (blastn)

Choose a BLAST algorithm [?]

- Megablast is intended for comparing a query to closely related sequences and works best if the target percent identity is 95% or more but is very fast.
- Discontiguous megablast uses an initial seed that ignores some bases (allowing mismatches) and is intended for cross-species comparisons.
- BlastN is slow, but allows a word-size down to seven bases.

more...

Algorithm

- ◯ blastp (protein-protein BLAST)

- ◯ PSI-BLAST (Position-Specific Iterated BLAST)

- ◯ PHI-BLAST (Pattern Hit Initiated BLAST)

Enter a PHI pattern [?]

Enter a PHI pattern to start the search. PHI-BLAST may perform better than simple pattern searching because it filters out false positives (pattern matches that are probably random and not indicative of homology).

Choose a BLAST algorithm [?]

- BlastP simply compares a protein query to a protein database.
- PSI-BLAST allows the user to build a PSSM (position-specific scoring matrix) using the results of the first BlastP run.)
- PHI-BLAST performs the search but limits alignments to those that match a pattern in the query.

BLAST

Search nucleotide sequenceusing Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window

Algorithm parameters

General Parameters

Max target sequences

| 100 ▾ |

Select the maximum number of aligned sequences to display [?]

Maximum number of aligned sequences to display (the actual number of alignments may be greater than this).

Short queries

☑ Automatically adjust parameters for short input sequences [?]

Automatically adjust word size and other parameters to improve results for short queries.

Expect threshold

| 10 | [?] |

Expected number of chance matches in a random model. more...

Word size
[11 ▼] [?]

The length of the seed that initiates an alignment. more...

Scoring Parameters

Matrix
[PAM30 ▼] [?]

Assigns a score for aligning pairs of residues, and determines overall alignment score. more...

Match/Mismatch Scores
[2,-3 ▼] [?]

Reward and penalty for matching and mismatching bases. more...

Gap Costs
[Existence: 5 Extension: 2 ▼] [?]

Cost to create and extend a gap in an alignment. Linear costs are available only with megablast and are determined by the match/mismatch scores. more...

Compositional adjustments
[No adjustment ▼] [?]

Matrix adjustment method to compensate for amino acid composition of sequences. more...

Filters and Masking

Filter
☑ Low complexity regions [?]

Mask regions of low compositional complexity that may cause spurious or misleading results. more...

☐ Species-specific repeats for: [Human ▼] [?]

Mask repeat elements of the specified species that may lead to spurious or misleading results. more...

Mask
☑ Mask for lookup table only [?]

Mask query while producing seeds used to scan database, but not for extensions. more...

☐ Mask lower case letters [?]

Mask any letters that were lower-case in the FASTA input. more...

Discontiguous Word Options

Template length

[18 ▼] [?]

Total number of bases in a seed that ignores some positions. more...

Template type

[Coding ▼] [?]

Specifies which bases are ignored in scanning the database. more...

PSI/PHI BLAST

PSSM

PSSM is uploaded... Clear

Upload PSSM Optional

[_____] [Browse...] [?]

Upload a Position Specific Score Matrix (PSSM) that you previously downloaded from a PSI-BLAST iteration. You may search a different database than that used to generate the PSSM, but you must use the same query. more...

PSI-BLAST Threshold

[_____] [?]

Set the statistical significance threshold to include a sequence in the model used by PSI-BLAST to create the PSSM on the next iteration.

[BLAST]

Search nucleotide sequenceusing Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window

[7 ▼] [28 ▼] [11 ▼] [Linear ▼] [Linear ▼] [Linear ▼] [Linear ▼]

[Linear ▼] [Existence: 5 Extension: 2 ▼]

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BLAST Basic Local Alignment Search Tool

- •

Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...

Results for: |ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp) ▒|
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
    gi|11545911|ref|NM_022162.1|
Description
    Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA
Molecule type
    rna
Query Length
    4485

Subject ID
    gi|14277249|gb|AC007728.4|AC007728
Description
    Homo sapiens chromosome 16 clone RP11-327F22, complete sequence
Molecule type
    nucleic acid
Subject Length
    168271
Program
    BLASTN 2.2.20+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string   L;m;
Genetic Code   1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 750722576

Graphic Summary

Distribution of 28 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

0   850   1700   2550   3400   4250
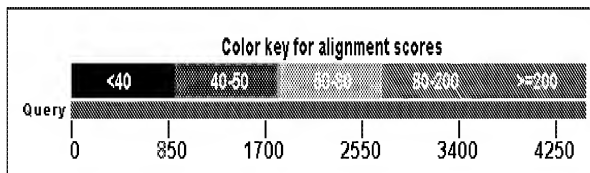
Dot Matrix View

Plot of gi|11545911|ref|NM_022162.1| vs gi|14277249|gb|AC007728.4|AC007728 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: ▨ UniGene ▨ GEO ▨ Gene ▨ Structure ▨ Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

AC007728.4	Homo sapiens chromosome 16 clone RP11-327F22, complete sequence	3279	8591	100%	0.0	100%

>gb|AC007728.4|AC007728   Homo sapiens chromosome 16 clone RP11-327F22, complete sequence
Length=168271

Sort alignments for this subject sequence by:
  E value **Score Percent identity**
  Query start position Subject start position

 Score = 3279 bits (3636), Expect = 0.0
 Identities = 1818/1818 (100%), Gaps = 0/1818 (0%)
 Strand=Plus/Minus

```
Query  750     AGCTGCCACATGCAAGAAGTATATGGCCAAGCTGAGGACCACGGTGTCTGCTCAGTCTCG  809
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140450  AGCTGCCACATGCAAGAAGTATATGGCCAAGCTGAGGACCACGGTGTCTGCTCAGTCTCG  140391

Query  810     CTTCCTCAGTACCTATGATGGAGCAGAGACGCTCTGCCTGGAGGACATATACACAGAGAA  869
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140390  CTTCCTCAGTACCTATGATGGAGCAGAGACGCTCTGCCTGGAGGACATATACACAGAGAA  140331

Query  870     TGTCCTGGAGGTCTGGGCAGATGTGGGCATGGCTGGACCCCCGCAGAAGAGCCCAGCCAC  929
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140330  TGTCCTGGAGGTCTGGGCAGATGTGGGCATGGCTGGACCCCCGCAGAAGAGCCCAGCCAC  140271

Query  930     CCTGGGCCTGGAGGAGCTCTTCAGCACCCCTGGCCACCTCAATGACGATGCGGACACTGT  989
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140270  CCTGGGCCTGGAGGAGCTCTTCAGCACCCCTGGCCACCTCAATGACGATGCGGACACTGT  140211

Query  990     GCTGGTGGTGGGTGAGGCGGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCT  1049
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140210  GCTGGTGGTGGGTGAGGCGGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCT  140151

Query  1050    GTGGGCTGCAGGGCAAGACTTCCAGGAATTTCTCTTTGTCTTCCCATTCAGCTGCCGGCA  1109
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140150  GTGGGCTGCAGGGCAAGACTTCCAGGAATTTCTCTTTGTCTTCCCATTCAGCTGCCGGCA  140091

Query  1110    GCTGCAGTGCATGGCCAAACCACTCTCTGTGCGGACTCTACTCTTTGAGCACTGCTGTTG  1169
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140090  GCTGCAGTGCATGGCCAAACCACTCTCTGTGCGGACTCTACTCTTTGAGCACTGCTGTTG  140031

Query  1170    GCCTGATGTTGGTCAAGAAGACATCTTCCAGTTACTCCTTGACCACCCTGACCGTGTCCT  1229
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140030  GCCTGATGTTGGTCAAGAAGACATCTTCCAGTTACTCCTTGACCACCCTGACCGTGTCCT  139971
```

```
Query  1230   GTTAACCTTTGATGGCTTTGACGAGTTCAAGTTCAGGTTCACGGATCGTGAACGCCACTG   1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139970  GTTAACCTTTGATGGCTTTGACGAGTTCAAGTTCAGGTTCACGGATCGTGAACGCCACTG   139911

Query  1290   CTCCCCGACCGACCCCACCTCTGTCCAGACCCTGCTCTTCAACCTTCTGCAGGGCAACCT   1349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139910  CTCCCCGACCGACCCCACCTCTGTCCAGACCCTGCTCTTCAACCTTCTGCAGGGCAACCT   139851

Query  1350   GCTGAAGAATGCCCGCAAGGTGGTGACCAGCCGTCCGGCCGCTGTGTCGGCGTTCCTCAG   1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139850  GCTGAAGAATGCCCGCAAGGTGGTGACCAGCCGTCCGGCCGCTGTGTCGGCGTTCCTCAG   139791

Query  1410   GAAGTACATCCGCACCGAGTTCAACCTCAAGGGCTTCTCTGAACAGGGCATCGAGCTGTA   1469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139790  GAAGTACATCCGCACCGAGTTCAACCTCAAGGGCTTCTCTGAACAGGGCATCGAGCTGTA   139731

Query  1470   CCTGAGGAAGCGCCATCATGAGCCCGGGGTGGCGGACCGCCTCATCCGCCTGCTCCAAGA   1529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139730  CCTGAGGAAGCGCCATCATGAGCCCGGGGTGGCGGACCGCCTCATCCGCCTGCTCCAAGA   139671

Query  1530   GACCTCAGCCCTGCACGGTTTGTGCCACCTGCCTGTCTTCTCATGGATGGTGTCCAAATG   1589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139670  GACCTCAGCCCTGCACGGTTTGTGCCACCTGCCTGTCTTCTCATGGATGGTGTCCAAATG   139611

Query  1590   CCACCAGGAACTGTTGCTGCAGGAgggggggTCCCCAAAGACCACTACAGATATGTACCT   1649
              |||||||||||||||||||||||||          ||||||||||||||||||||||||||
Sbjct  139610  CCACCAGGAACTGTTGCTGCAGGAGGGGGGGGGTCCCCAAAGACCACTACAGATATGTACCT   139551

Query  1650   GCTGATTCTGCAGCATTTTCTGCTGCATGCCcccccccAGACTCAGCTTCCCAAGGTCT   1709
              ||||||||||||||||||||||||||||||         |||||||||||||||||||||
Sbjct  139550  GCTGATTCTGCAGCATTTTCTGCTGCATGCCCACCCCCCCAGACTCAGCTTCCCAAGGTCT   139491

Query  1710   GGGACCCAGTCTTCTTCGGGGCCGCCTCCCCACCCTCCTGCACCTGGGCAGACTGGCTCT   1769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139490  GGGACCCAGTCTTCTTCGGGGCCGCCTCCCCACCCTCCTGCACCTGGGCAGACTGGCTCT   139431

Query  1770   GTGGGGCCTGGGCATGTGCTGCTACGTGTTCTCAGCCCAGCAGCTCCAGGCAGCACAGGT   1829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139430  GTGGGGCCTGGGCATGTGCTGCTACGTGTTCTCAGCCCAGCAGCTCCAGGCAGCACAGGT   139371

Query  1830   CAGCCCTGATGACATTTCTCTTGGCTTCCTGGTGCGTGCCAAAGGTGTCGTGCCAGGGAG   1889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139370  CAGCCCTGATGACATTTCTCTTGGCTTCCTGGTGCGTGCCAAAGGTGTCGTGCCAGGGAG   139311

Query  1890   TACGGCGCCCCTGGAATTCCTTCACATCACTTTCCAGTGCTTCTTTGCCGCGTTCTACCT   1949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139310  TACGGCGCCCCTGGAATTCCTTCACATCACTTTCCAGTGCTTCTTTGCCGCGTTCTACCT   139251

Query  1950   GGCACTCAGTGCTGATGTGCCACCAGCTTTGCTCAGACACCTCTTCAATTGTGGCAGGCC   2009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139250  GGCACTCAGTGCTGATGTGCCACCAGCTTTGCTCAGACACCTCTTCAATTGTGGCAGGCC   139191

Query  2010   AGGCAACTCACCAATGGCCAGGCTCCTGCCCACGATGTGCATCCAGGCCTCGGAGGGAAA   2069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139190  AGGCAACTCACCAATGGCCAGGCTCCTGCCCACGATGTGCATCCAGGCCTCGGAGGGAAA   139131

Query  2070   GGACAGCAGCGTGGCAGCTTTGCTGCAGAAGGCCGAGCCGCACAACCTTCAGATCACAGC   2129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139130  GGACAGCAGCGTGGCAGCTTTGCTGCAGAAGGCCGAGCCGCACAACCTTCAGATCACAGC   139071

Query  2130   AGCCTTCCTGGCAGGGCTGTTGTCCCGGGAGCACTGGGGCCTGCTGGCTGAGTGCCAGAC   2189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Sbjct  139070  AGCCTTCCTGGCAGGGCTGTTGTCCCGGGAGCACTGGGGCCTGCTGGCTGAGTGCCAGAC  139011

Query  2190    ATCTGAGAAGGCCCTGCTCCGGCGCCAGGCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCT  2249
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139010  ATCTGAGAAGGCCCTGCTCCGGCGCCAGGCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCT  138951

Query  2250    CCGCAAGCACTTCCACTCCATCCCGCCAGCTGCACCGGGTGAGGCCAAGAGCGTGCATGC  2309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138950  CCGCAAGCACTTCCACTCCATCCCGCCAGCTGCACCGGGTGAGGCCAAGAGCGTGCATGC  138891

Query  2310    CATGCCCGGGTTCATCTGGCTCATCCGGAGCCTGTACGAGATGCAGGAGGAGCGGCTGGC  2369
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138890  CATGCCCGGGTTCATCTGGCTCATCCGGAGCCTGTACGAGATGCAGGAGGAGCGGCTGGC  138831

Query  2370    TCGGAAGGCTGCACGTGGCCTGAATGTTGGGCACCTCAAGTTGACATTTTGCAGTGTGGG  2429
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138830  TCGGAAGGCTGCACGTGGCCTGAATGTTGGGCACCTCAAGTTGACATTTTGCAGTGTGGG  138771

Query  2430    CCCCACTGAGTGTGCTGCCCTGGCCTTTGTGCTGCAGCACCTCCGGCGGCCCGTGGCCCT  2489
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138770  CCCCACTGAGTGTGCTGCCCTGGCCTTTGTGCTGCAGCACCTCCGGCGGCCCGTGGCCCT  138711

Query  2490    GCAGCTGGACTACAACTCTGTGGGTGACATTGGCGTGGAGCAGCTGCTGCCTTGCCTTGG  2549
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138710  GCAGCTGGACTACAACTCTGTGGGTGACATTGGCGTGGAGCAGCTGCTGCCTTGCCTTGG  138651

Query  2550    TGTCTGCAAGGCTCTGTA  2567
               ||||||||||||||||||
Sbjct  138650  TGTCTGCAAGGCTCTGTA  138633


 Score = 2401 bits (2662),  Expect = 0.0
 Identities = 1331/1331 (100%), Gaps = 0/1331 (0%)
 Strand=Plus/Minus

Query  3155    GGCTCCGAGGGAACACTTTCTCTCTAGAGGAGGTTGACAAGCTCGGCTGCAGGGACACCA  3214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119260  GGCTCCGAGGGAACACTTTCTCTCTAGAGGAGGTTGACAAGCTCGGCTGCAGGGACACCA  119201

Query  3215    GACTCTTGCTTTGAAGTCTCCGGGAGGATGTTCGTCTCAGTTTGTTTGTGAGCAGGCTGT  3274
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119200  GACTCTTGCTTTGAAGTCTCCGGGAGGATGTTCGTCTCAGTTTGTTTGTGAGCAGGCTGT  119141

Query  3275    GAGTTTGGGCCCCAGAGGCTGGGTGACATGTGTTGGCAGCCTCTTCAAAATGAGCCCTGT  3334
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119140  GAGTTTGGGCCCCAGAGGCTGGGTGACATGTGTTGGCAGCCTCTTCAAAATGAGCCCTGT  119081

Query  3335    CCTGCCTAAGGCTGAACTTGTTTTCTGGGAACACCATAGGTCACCTTTATTCTGGCAGAG  3394
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119080  CCTGCCTAAGGCTGAACTTGTTTTCTGGGAACACCATAGGTCACCTTTATTCTGGCAGAG  119021

Query  3395    GAGGGAGCATCAGTGCCCTCCAGGATAGACTTTTCCCAAGCCTACTTTTGCCATTGACTT  3454
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119020  GAGGGAGCATCAGTGCCCTCCAGGATAGACTTTTCCCAAGCCTACTTTTGCCATTGACTT  118961

Query  3455    CTTCCCAAGATTCAATCCCAGGATGTACAAGGACAGCCCCTCCTCCATAGTATGGGACTG  3514
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  118960  CTTCCCAAGATTCAATCCCAGGATGTACAAGGACAGCCCCTCCTCCATAGTATGGGACTG  118901

Query  3515    GCCTCTGCTGATCCTCCCAGGCTTCCGTGTGGGTCAGTGGGGCCCATGGATGTGCTTGTT  3574
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  118900  GCCTCTGCTGATCCTCCCAGGCTTCCGTGTGGGTCAGTGGGGCCCATGGATGTGCTTGTT  118841
```

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Query   3575   AACTGAGTGCCTTTTGGTGGAGAGGCCCGGCCTCTCACAAAAGACCCCTTACCACTGCTC   3634
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118840  AACTGAGTGCCTTTTGGTGGAGAGGCCCGGCCTCTCACAAAAGACCCCTTACCACTGCTC   118781

Query   3635   TGATGAAGAGGAGTACACAGAACACATAATTCAGGAAGCAGCTTTCCCCATGTCTCGACT   3694
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118780  TGATGAAGAGGAGTACACAGAACACATAATTCAGGAAGCAGCTTTCCCCATGTCTCGACT   118721

Query   3695   CATCCATCCAGGCCATTCCCCGTCTCTGGTTCCTCCCCTCCTCCTGGACTCCTGCACACG   3754
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118720  CATCCATCCAGGCCATTCCCCGTCTCTGGTTCCTCCCCTCCTCCTGGACTCCTGCACACG   118661

Query   3755   CTCCTTCCTCTGAGGCTGAAATTCAGAATATTAGTGACCTCAGCTTTGATATTTCACTTA   3814
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118660  CTCCTTCCTCTGAGGCTGAAATTCAGAATATTAGTGACCTCAGCTTTGATATTTCACTTA   118601

Query   3815   CAGCACCCCCAACCCTGGCACCCAGGGTGGGAAGGGCTACACCTTAGCCTGCCCTCCTTT   3874
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118600  CAGCACCCCCAACCCTGGCACCCAGGGTGGGAAGGGCTACACCTTAGCCTGCCCTCCTTT   118541

Query   3875   CCGGTGTTTAAGACATTTTTGGAAGGGGACACGTGACAGCCGTTTGTTCCCCAAGACATT   3934
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118540  CCGGTGTTTAAGACATTTTTGGAAGGGGACACGTGACAGCCGTTTGTTCCCCAAGACATT   118481

Query   3935   CTAGGTTTGCAAGAAAAATATGACCACACTCCAGCTGGGATCACATGTGGACTTTTATTT   3994
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118480  CTAGGTTTGCAAGAAAAATATGACCACACTCCAGCTGGGATCACATGTGGACTTTTATTT   118421

Query   3995   CCAGTGAAATCAGTTACTCTTCAGTTAAGCCTTTGGAAACAGCTCGACTTTAAAAAGCTC   4054
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118420  CCAGTGAAATCAGTTACTCTTCAGTTAAGCCTTTGGAAACAGCTCGACTTTAAAAAGCTC   118361

Query   4055   CAAATGCAGCTTTAAAAAATTAATCTGGGCCAGAATTTCAAACGGCCTCACTAGGCTTCT   4114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118360  CAAATGCAGCTTTAAAAAATTAATCTGGGCCAGAATTTCAAACGGCCTCACTAGGCTTCT   118301

Query   4115   GGTTGATGCCTGTGAACTGAACTCTGACAACAGACTTCTGAAATAGACCCACAAGAGGCA   4174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118300  GGTTGATGCCTGTGAACTGAACTCTGACAACAGACTTCTGAAATAGACCCACAAGAGGCA   118241

Query   4175   GTTCCATTTCATTTGTGCCAGAATGCTTTAGGATGTACAGTTATGGATTGAAAGTTTACA   4234
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118240  GTTCCATTTCATTTGTGCCAGAATGCTTTAGGATGTACAGTTATGGATTGAAAGTTTACA   118181

Query   4235   GGaaaaaaaaTTAGGCCGTTCCTTCAAAGCAAATGTCTTCCTGGATTATTCAAAATGATG   4294
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118180  GGAAAAAAAATTAGGCCGTTCCTTCAAAGCAAATGTCTTCCTGGATTATTCAAAATGATG   118121

Query   4295   TATGTTGAAGCCTTTGTAAATTGTCAGATGCTGTGCAAATGTTATTATTTTAAACATTAT   4354
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118120  TATGTTGAAGCCTTTGTAAATTGTCAGATGCTGTGCAAATGTTATTATTTTAAACATTAT   118061

Query   4355   GATGTGTGAAAACTGGTTAATATTTATAGGTCACTTTGTTTTACTGTCTTAAGTTTATAC   4414
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118060  GATGTGTGAAAACTGGTTAATATTTATAGGTCACTTTGTTTTACTGTCTTAAGTTTATAC   118001

Query   4415   TCTTATAGACAACATGGCCGTGAACTTTATGCTGTAAATAATCAGAGGGGAATAAACTGT   4474
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   118000  TCTTATAGACAACATGGCCGTGAACTTTATGCTGTAAATAATCAGAGGGGAATAAACTGT   117941

Query   4475   TGAGTCAAAAC   4485
               |||||||||||
Sbjct   117940  TGAGTCAAAAC   117930
```

```
 Score =  848 bits (940),  Expect = 0.0
 Identities = 473/475 (99%), Gaps = 0/475 (0%)
 Strand=Plus/Minus

Query  172    TCTCCGGGTTGTGAAATGTGCTCGCAGGAGGCTTTTCAGGCACAGAGGAGCCAGCTGGTC  231
              || ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151525  TCCCCAGGTTGTGAAATGTGCTCGCAGGAGGCTTTTCAGGCACAGAGGAGCCAGCTGGTC  151466

Query  232    GAGCTGCTGGTCTCAGGGTCCCTGGAAGGCTTCGAGAGTGTCCTGGACTGGCTGCTGTCC  291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151465  GAGCTGCTGGTCTCAGGGTCCCTGGAAGGCTTCGAGAGTGTCCTGGACTGGCTGCTGTCC  151406

Query  292    TGGGAGGTCCTCTCCTGGGAGGACTACGAGGGCTTCCACCTCCTGGGCCAGCCTCTCTCC  351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151405  TGGGAGGTCCTCTCCTGGGAGGACTACGAGGGCTTCCACCTCCTGGGCCAGCCTCTCTCC  151346

Query  352    CACTTGGCCAGGCGCCTTCTGGACACCGTCTGGAATAAGGGTACTTGGGCCTGTCAGAAG  411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151345  CACTTGGCCAGGCGCCTTCTGGACACCGTCTGGAATAAGGGTACTTGGGCCTGTCAGAAG  151286

Query  412    CTCATCGCGGCTGCCCAAGAAGCCCAGGCCGACAGCCAGTCCCCCAAGCTGCATGGCTGC  471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151285  CTCATCGCGGCTGCCCAAGAAGCCCAGGCCGACAGCCAGTCCCCCAAGCTGCATGGCTGC  151226

Query  472    TGGGACCCCCACTCGCTCCACCCAGCCCGAGACCTGCAGAGTCACCGGCCAGCCATTGTC  531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151225  TGGGACCCCCACTCGCTCCACCCAGCCCGAGACCTGCAGAGTCACCGGCCAGCCATTGTC  151166

Query  532    AGGAGGCTCCACAGCCATGTGGAGAACATGCTGGACCTGGCATGGGAGCGGGGTTTCGTC  591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151165  AGGAGGCTCCACAGCCATGTGGAGAACATGCTGGACCTGGCATGGGAGCGGGGTTTCGTC  151106

Query  592    AGCCAGTATGAATGTGATGAAATCAGGTTGCCGATCTTCACACCGTCCCAGAGGG  646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151105  AGCCAGTATGAATGTGATGAAATCAGGTTGCCGATCTTCACACCGTCCCAGAGGG  151051


 Score =  325 bits (360),  Expect = 6e-90
 Identities = 180/180 (100%), Gaps = 0/180 (0%)
 Strand=Plus/Minus

Query  1      GTAGACAGATCCAGGCTCACCAGTCCTGTGCCACTGGGCTTTTGGCGTTCTGCACAAGGC  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  153867  GTAGACAGATCCAGGCTCACCAGTCCTGTGCCACTGGGCTTTTGGCGTTCTGCACAAGGC  153808

Query  61     CTACCCGCAGATGCCATGCCTGCTCCCCCAGCCTAATGGGCTTTGATGGGGGAAGAGGGT  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  153807  CTACCCGCAGATGCCATGCCTGCTCCCCCAGCCTAATGGGCTTTGATGGGGGAAGAGGGT  153748

Query  121    GGTTCAGCCTCTCACGATGAGGAGGAAAGAGCAAGTGTCCTCCTCGGACATTCTCCGGGT  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  153747  GGTTCAGCCTCTCACGATGAGGAGGAAAGAGCAAGTGTCCTCCTCGGACATTCTCCGGGT  153688


 Score =  194 bits (214),  Expect = 3e-50
 Identities = 107/107 (100%), Gaps = 0/107 (0%)
 Strand=Plus/Minus

Query  645    GGCAAGAAGGCTGCTTGATCTTGCCACGGTGAAAGCGAATGGATTGGCTGCCTTCCTTCT  704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  143152  GGCAAGAAGGCTGCTTGATCTTGCCACGGTGAAAGCGAATGGATTGGCTGCCTTCCTTCT  143093
```

```
Query  705    ACAACATGTTCAGGAATTACCAGTCCCATTGGCCCTGCCTTTGGAAG  751
              |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  143092 ACAACATGTTCAGGAATTACCAGTCCCATTGGCCCTGCCTTTGGAAG  143046
```

 Score = 158 bits (174), Expect = 2e-39
 Identities = 87/87 (100%), Gaps = 0/87 (0%)
 Strand=Plus/Minus

```
Query  2987   GCCTGGAGGAGAACCATCTCCAGGATGAAGGTGTATGTTCTCTCGCAGAAGGACTGAAGA  3046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  125518 GCCTGGAGGAGAACCATCTCCAGGATGAAGGTGTATGTTCTCTCGCAGAAGGACTGAAGA  125459

Query  3047   AAAATTCAAGTTTGAAAATCCTGAAGT  3073
              |||||||||||||||||||||||||||
Sbjct  125458 AAAATTCAAGTTTGAAAATCCTGAAGT  125432
```

 Score = 158 bits (174), Expect = 2e-39
 Identities = 87/87 (100%), Gaps = 0/87 (0%)
 Strand=Plus/Minus

```
Query  2901   CAGCCTGGTGGGGAACAACATTGGCAGTGTGGGTGCCCAAGCCTTGGCACTGATGCTGGC  2960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  127708 CAGCCTGGTGGGGAACAACATTGGCAGTGTGGGTGCCCAAGCCTTGGCACTGATGCTGGC  127649

Query  2961   AAAGAACGTCATGCTAGAAGAACTCTG  2987
              |||||||||||||||||||||||||||
Sbjct  127648 AAAGAACGTCATGCTAGAAGAACTCTG  127622
```

 Score = 156 bits (172), Expect = 6e-39
 Identities = 86/86 (100%), Gaps = 0/86 (0%)
 Strand=Plus/Minus

```
Query  2734   AGGCTGGGGAATAACTACATCACTGCCGCGGGAGCCCAAGTGCTGGCCGAGGGGCTCCGA  2793
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131083 AGGCTGGGGAATAACTACATCACTGCCGCGGGAGCCCAAGTGCTGGCCGAGGGGCTCCGA  131024

Query  2794   GGCAACACCTCCTTGCAGTTCCTGGG  2819
              ||||||||||||||||||||||||||
Sbjct  131023 GGCAACACCTCCTTGCAGTTCCTGGG  130998
```

 Score = 154 bits (170), Expect = 2e-38
 Identities = 85/85 (100%), Gaps = 0/85 (0%)
 Strand=Plus/Minus

```
Query  3072   GTTGTCCAATAACTGCATCACCTACCTAGGGGCAGAAGCCCTCCTGCAGGCCCTTGAAAG  3131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121188 GTTGTCCAATAACTGCATCACCTACCTAGGGGCAGAAGCCCTCCTGCAGGCCCTTGAAAG  121129

Query  3132   GAATGACACCATCCTGGAAGTCTGG  3156
              |||||||||||||||||||||||||
Sbjct  121128 GAATGACACCATCCTGGAAGTCTGG  121104
```

 Score = 154 bits (170), Expect = 2e-38
 Identities = 85/85 (100%), Gaps = 0/85 (0%)
 Strand=Plus/Minus

```
Query  2819   GATTCTGGGGCAACAGAGTGGGTGACGAGGGGGCCCAGGCCCTGGCTGAAGCCTTGGGTG  2878
```

```
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  128385    GATTCTGGGGCAACAGAGTGGGTGACGAGGGGGCCCAGGCCCTGGCTGAAGCCTTGGGTG  128326

Query  2879      ATCACCAGAGCTTGAGGTGGCTCAG  2903
                 |||||||||||||||||||||||||
Sbjct  128325    ATCACCAGAGCTTGAGGTGGCTCAG  128301


 Score =  154 bits (170),  Expect = 2e-38
 Identities = 85/85 (100%), Gaps = 0/85 (0%)
 Strand=Plus/Minus

Query  2652      TCTATTCAACAACAAATTGACTGACGGCTGTGCACACTCCATGGCTAAGCTCCTTGCATG  2711
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134115    TCTATTCAACAACAAATTGACTGACGGCTGTGCACACTCCATGGCTAAGCTCCTTGCATG  134056

Query  2712      CAGGCAGAACTTCTTGGCATTGAGG  2736
                 |||||||||||||||||||||||||
Sbjct  134055    CAGGCAGAACTTCTTGGCATTGAGG  134031


 Score =  154 bits (170),  Expect = 2e-38
 Identities = 90/92 (97%), Gaps = 1/92 (1%)
 Strand=Plus/Minus

Query  2561      CTCTGTA-TTTGCGCGATAACAATATCTCAGACCGAGGCATCTGCAAGCTCATTGAATGT  2619
                 ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134427    CTCTTTAGTTTGCGCGATAACAATATCTCAGACCGAGGCATCTGCAAGCTCATTGAATGT  134368

Query  2620      GCTCTTCACTGCGAGCAATTGCAGAAGTTAGC  2651
                 ||||||||||||||||||||||||||||||||
Sbjct  134367    GCTCTTCACTGCGAGCAATTGCAGAAGTTAGC  134336


 Score =  35.6 bits (38),  Expect = 0.015
 Identities = 22/24 (91%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

Query  4221      ATTGAAAGTTTACAGGaaaaaaaa  4244
                 ||| | |||||||||||||||||
Sbjct  60530     ATTAACAGTTTACAGGAAAAAAAA  60553


 Score =  30.1 bits (32),  Expect = 0.63
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Plus

Query  281       GGCTGCTGTCCTGGGAGGT  299
                 ||| |||||||||||||||
Sbjct  131339    GGCAGCTGTCCTGGGAGGT  131357


 Score =  30.1 bits (32),  Expect = 0.63
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  339       CCAGCCTCTCTCCCACTTG  357
                 || ||||||||||||||||
Sbjct  136285    CCTGCCTCTCTCCCACTTG  136267


 Score =  30.1 bits (32),  Expect = 0.63
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
```

```
   Strand=Plus/Plus

 Query  1098     CAGCTGCCGGCAGCTG  1113
                 ||||||||||||||||
 Sbjct  140087   CAGCTGCCGGCAGCTG  140102


 Score = 28.3 bits (30),  Expect = 2.2
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

 Query  2801  CCTCCTTGCAGTTCC  2815
              |||||||||||||||
 Sbjct  8417  CCTCCTTGCAGTTCC  8403


 Score = 28.3 bits (30),  Expect = 2.2
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

 Query  953     GCACCCCTGGCCACC  967
                |||||||||||||||
 Sbjct  109718  GCACCCCTGGCCACC  109732


 Score = 28.3 bits (30),  Expect = 2.2
 Identities = 21/25 (84%), Gaps = 0/25 (0%)
 Strand=Plus/Plus

 Query  2283    ACCGGGTGAGGCCAAGAGCGTGCAT  2307
                || || ||||  |||||||||||||
 Sbjct  160465  ACAGGCTGAGTGCAAGAGCGTGCAT  160489


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

 Query  1064  AAGACTTCCAGGAA  1077
              ||||||||||||||
 Sbjct  1485  AAGACTTCCAGGAA  1472


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 26/34 (76%), Gaps = 0/34 (0%)
 Strand=Plus/Minus

 Query  1608   GCAGGAgggggggTCCCCAAAGACCACTACAGAT  1641
               ||||||||   ||||| ||  ||||||||||
 Sbjct  10423  GCAGGAGGTCCTGTCCCTCAAACCCACTACAGAT  10390


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

 Query  3051   TTCAAGTTTGAAAA  3064
               ||||||||||||||
 Sbjct  68988  TTCAAGTTTGAAAA  69001


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
```

```
  Strand=Plus/Plus

 Query  4154   GAAATAGACCCACA  4167
               ||||||||||||||
 Sbjct  79121  GAAATAGACCCACA  79134


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

 Query  3807   TTCACTTACAGCAC  3820
               ||||||||||||||
 Sbjct  120449 TTCACTTACAGCAC  120462


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

 Query  2983   CTCTGCCTGGAGGA  2996
               ||||||||||||||
 Sbjct  140359 CTCTGCCTGGAGGA  140346


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

 Query  3015   AGGTGTATGTTCTC  3028
               ||||||||||||||
 Sbjct  143043 AGGTGTATGTTCTC  143030


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 17/19 (89%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

 Query  4060   GCAGCTTTAAAAAATTAAT  4078
               ||| ||||||||||| |||
 Sbjct  160764 GCATCTTTAAAAAATAAAT  160746


 Score = 26.5 bits (28),  Expect = 7.7
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

 Query  3015   AGGTGTATGTTCTC  3028
               ||||||||||||||
 Sbjct  164997 AGGTGTATGTTCTC  165010
```

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